

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

April 29, 2001, 06:40:29 ; Search time 14.58 Seconds

(without alignments)
608.042 Million cell updates/sec

Title: US-09-726-899-3
Perfect score: 678
Sequence: 1 MSFPKYKPSSLRTLPEFLDP..... DRKEKLIQEGKLDRTRFFHLSY 129
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_67:*

1: pir1,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	1
Query	JE0383
Best Match	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFB4 - human
Local Similarity	100 %;
Matches	129;
Conservative	0;
Pred. No.	6.1e-65;
Mismatches	0;
Indels	0;
Gaps	0;

Description

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFB4 - human
C; Species: Homo sapiens (man)
C; Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C; Accession: JE0383
R; Loeffen, J.J.C.M.; Triespel, R.H.; van den Heuvel, L.P.; Schuelke, M.; Buskens, C.A.
Blochem. Biophys. Res. Commun. 253, 415-422, 1998
A; Title: cDNA of eight nuclear encoded subunits of NADH:ubiquinone oxidoreductase: Hu
A; Reference number: JE0379; MUID:99097250
A; Accession: JE0383
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-129 <LOC>
A; Cross-references: GB:AB044957; NID:9164445; PIDN:AA05421.1; PID:9416446
C; Keywords: NAD; oxidoreductase

Query	Match	Score	DB	Length
QY	1 MSFPKYKPSSLRTLPEFLDP..... DRKEKLIQEGKLDRTRFFHLSY 129	678	2	129;
Db	1 MSFPKYKPSSLRTLPEFLDP..... DRKEKLIQEGKLDRTRFFHLSY 129	60	2	129;
QY	61 ENPALLRWAVARTINVYPNFRPTPRNSLMLGACGGGPLFLFVYIYIKTERDRKEKLIQEK 120	61	2	120;
Db	61 ENPALLRWAVARTINVYPNFRPTPRNSLMLGACGGGPLFLFVYIYIKTERDRKEKLIQEK 120	60	2	120;
QY	121 LDRTFILSY 129	61	2	120;
Db	121 LDRTFILSY 129	60	2	120;

RESULT 2

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain B15 - bovine
C; Species: Bos primigenius taurus (cattle)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C; Accession: S28237
R; Walker, J.E.; Arizmendi, J.M.; Dupuis, A.; Fearnley, I.M.; Finel, M.; Medd, S.M.; P
J. Mol. Biol. 226, 1051-1072, 1992
A; Title: Sequences of 20 subunits of NADH: ubiquinone oxidoreductase from bovine heart
A; Reference number: S28237; MUID:92389317
A; Accession: S28237
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-129 <VAL>
A; Cross-references: EMBL:X64898; NID:9113; PIDN:CAA46107.1; PID:9114
C; Keywords: electron transfer; mitochondrion; NAD; oxidoreductase

30	66.5	9.8	472	2	B37777
31	66.5 <th>9.8</th> <td>634</td> <td>2</td> <td>E83263</td>	9.8	634	2	E83263
32	66.5 <th>9.8</th> <td>674</td> <td>2</td> <td>S32230</td>	9.8	674	2	S32230
33	66.5 <th>9.8</th> <td>1036</td> <td>2</td> <td>A57386</td>	9.8	1036	2	A57386
34	66 <td>9.7</td> <td>193</td> <td>2</td> <td>H81874</td>	9.7	193	2	H81874
35	66 <td>9.7</td> <td>271</td> <td>2</td> <td>T24965</td>	9.7	271	2	T24965
36	66	9.7	342	2	D71324
37	66	9.7	353	2	F83570
38	66	9.7	413	2	H75357
39	66	9.7	657	1	FOVZV
40	66	9.7	554	1	S54561
41	65.5	9.7	354	2	T22108
42	65.5	9.7	899	2	B38529
43	65.5	9.7	899	2	D83339
44	65.5	9.7	2358	2	T39569
45	65.5	9.7	2371	2	T43432

C;Genetics:
A;Gene: PA4331

Query	Match	Best Local Similarity	Score	No.	DB	Length:
Oy	TLPETLDPPAEVNTSPERTRQAERLATRAKQLKRYLQNDPNRGRGLEINPALLRW	35.7%	74	2	2	308
Db	TLPEDAIP-----VRREAGWRLAQOCRVLGDLVLOPFPDPERDGPLPARVACHW	20	5	Mismatches	23	Indels
					8	Gaps
						14

tryptophan synthase, chain beta (trpb-2) PAB1970 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75177
R;Synonyms: Genoscope
S;Submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: F75177
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <KAW>
A;Cross-references: GB:AU248284; GB:AU096836; NID:95457730; PIDN:CAB49501.1; PID:9545801
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1970
C;Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology <YSB>
F;29-432/Domain: tryptophan synthase beta chain homology

A;Residues: 1-695 <BUL>
A;Cross References: GB:U67478; GB:L77117; NID:91590958; PIDN:AAB98208.1; PID:91590966
C;Genetics:
A;Map position: RWM214151-212064
A;Start codon: GTG
C;Keywords: hydrolase

Matches	29;	Conservative	10;	Mismatches	26;	Indels	24;	Gaps	5
Qy	11	LRTLPETLDAEYNISET-----RRAQERLARLTAQLKREYLQYNDPNRRGLIE	61						
Db	29	LPLDPLPELPP---LDPETEEPIDIEKLKRIFAEEL-VKQEISRE--RY-----IE	73						
Qy	62	NPALLRAYATINVYNNFRPPPKNSLMG	90						
Db	74	IPGELRKLYSKIGRPTPLFRATNLEKLG	102						

dna protein - *Synechocystis* sp. (strain PCC 6803);
N; Alternate names: protein sl1932
C; Species: *Synechocystis* sp.

RESULT 10
T8376 multidrug resistance protein 2 - malaria parasite (*Plasmodium falciparum*)
C.Species: *Plasmodium falciparum*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okamura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, S.; DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A; Reference number: ST4322; MUID:97061201
A; Accession: S75209
A; Status: nucleic acid sequence not shown; translation not shown

N;Cross-references: EMBL:D9903; GB:AB01339; NID:9165127; PIDN:BA17123.1; PID:9165219
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: dnak
A;Start codon: GTG
C;Superfamily: heat shock protein 70

Query Match 10.3%; Score 70; DB 2; Length 1025;

Best Local Similarity 33.3%; Pred. No. 35; Matches 14; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

RESULT 11
S22440 protein kinase (EC 2.7.1.37) cdc2 homolog 1 ~ rice
C;Species: Oryza sativa (rice)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: S22440
R;Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzuki, I.; Utsugi, M.; Gen. Genet. 233, 10-16, 1992
A;Title: Isolation and characterization of cDNA clones encoding cdc2 homologues from rice
A;Database number: S22440; MUID:92293101
A;Position: S22440
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1294 <HAS>
A;Cross-references: EMBL:X53286; NID:9297084; PIDN:CAA42922.1; PID:920343
A;Cross-references: EMBL:X60374; NID:920342; PIDN:CAA42922.1; PID:920343
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;2-256/Domain: protein kinase homology <KIN>
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 10.3%; Score 69.5; DB 2; Length 294; Matches 36; Conservative 17; Mismatches 20; Indels 1; Gaps 1;

QY 2 SFPKYKPSSLRTIPEETDPAEYNISPETTERRAGAERLAIRAGLKEY 47
Db 240 AFPKWQAQDLATVPTLDPAGLDLISKMLRYEPNKRITARQALEHEY 286

RESULT 12
S65523 hypothetical protein 17 - phage HP1

C;Species: phage HP1
C;Accession: S65523
R;Pessino, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca, N.; Acids Res. 24, 2360-2368, 1996
A;Title: The complete nucleotide sequence of bacteriophage HP1 DNA.
A;Reference number: S65503; MUID:96219738
A;Accession: S65523
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1298 <ESP>
A;Cross-references: EMBL:U24159; NID:91046235; PIDN:AAB09202.1; PID:91046244
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

Query Match 10.2%; Score 69; DB 2; Length 298; Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

DB 143 ---ERIKVDESAKE-VEEEKALRT 163

RESULT 13
S12519 glutactin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: S12519

R;Olson, P.F.; Fessler, L.I.; Nelson, R.E.; Campbell, A.G.; Fessler, J.
EMBO J. 9, 1219-1227, 1990

A;Title: Glutactin, a novel *Drosophila* basement membrane-related glycoprotein with se

A;Reference number: S12519; MUID:90214632
A;Accession: S12519

A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <OLS>
A;Cross-references: EMBL:X53286; NID:9297084; PIDN:CAA37380.1; PID:9297085
A;Introns: 390/3

Query Match 10.2%; Score 69; DB 2; Length 1023; Matches 36; Conservative 15; Mismatches 45; Indels 40; Gaps 8;

QY 2 SFPKYKPSSLRTIPEETDPAEYNISPETTERRAGAERLAIRAGLKEY 47
Db 790 SYEOYGPBGENLNLPET---DANIRNSSEEDREQQEQEQRQEQEYQLOERQERQ 847

QY 53 DPNRRLGTE-NPALLRWAYARTINVYPNFRP----TPKNSIMGALCGFGGPLIFTYIK 106
Db 848 EDQERGQGP-----EYPSYEESRALQENKAERDRI-----YAEF 886

QY 107 TERDR--REKLOEGK 120
Db 887 QERBRQQQETLQENQ 902

RESULT 14
T88561 vitellogenin vit-6 [similarity] - *Oscheius* sp. (strain CEW1)

C;Species: *Oscheius* sp.
A;Variety: PsII131

C;Accession: T18561
C;Accession: T18561
R;Winter, C.E.; Penha, C.; Blumenthal, T.

Mol. Biol. Evol. 13, 644-654, 1996

A;Title: Comparison of a vitellogenin gene between two distantly related rhabditid ne

A;Reference number: Z18974; MUID:96212989
A;Accession: T18561

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
A;Residues: 1-1660 <WNT>

A;Cross-references: EMBL:U35449; NID:91515336; PID:91515337; PIDN:AAB49749.1
C;Genetics:
A;Introns: 28/1; 100/3; 171/3; 791/1
A;Note: CEW1-vit-6

C;Superfamily: vitellogenin
Query Match 10.2%; Score 69; DB 2; Length 1660; Matches 34; Conservative 20; Mismatches 57; Indels 26; Gaps 4;
QY 11 LRTLPLTDPLDAEY--NTSPETR--AQAERLATRAQLKR-YLQYNDPNRRGLIENP 63
Db 30 LHEMAEDYDPHEYTANWNPHEHRWFENNGQVTELKAEENEKGETQLIAAPNE-LIEYN 88

QY 64 ALLRWAVARTINVYPNFRPTPKNSL-----MGALCGGPLI 99
Db 83 RAGQYLFT-SIETPWNFRNSKGAYLGLGVTDSPASVGTTELKFENAEQKGSVCG---- 142

QY 100 FIYIYIKTERKEKLIQEGLKDRT 124
Db 687 LNWA----TFFSNISVLPEITASLETVGGEWKYLQAGLQNLDSVLSKLUQVE 741

QY 109 RDRKEKUHQEGKUDRPF 125
 | :| : | :| :|
 Db 742 ETCGLEOLVVRGKRSSF 758

RESULT 15

S23095 protein kinase (EC 2.7.1.37) cdc2 - *Arabidopsis thaliana* 2
 N; Alternative names: cdc2 protein homolog; CDC2a protein; cell division control protein 2
 C; Species: *Arabidopsis thaliana* (mouse-ear cress)
 C; Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
 C; Accession: S23095; A48984; JO1337; JQ0967; SI8202
 R; Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.
 FEBS Lett. 364, 73-77, 1992
 A; Reference number: S23095; MUID:92316202
 A; Accession: S23095
 A; Molecule type: DNA
 A; Residues: 1-294 <IM>
 A; Cross references: EMBL:DI0850; PIDN:9217848; PIDN:BAA01623.1; PID:9217849
 R; Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.
 Biotam. Soc. Trans. 20, 80-84, 1992
 A; Title: Control of cell division in Plants.
 A; Reference number: A48984; MUID:92339744
 A; Accession: A48984
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: nucleic acid
 A; Residues: 1-294 <INZ>
 A; Experimental source: flower
 A; Note: sequence extracted from NCBI backbone (NCBIP:109461)
 R; Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.
 Gene 105, 159-165, 1991
 Gene 105, 159-165, 1991
 Plant Cell 3, 531-540, 1991
 A; Title: Identification of two cell-cycle-controlling cdc2 gene homologs in *Arabidopsis*
 A; Reference number: JO1337; MUID:92039027
 A; Accession: JO1337
 A; Molecule type: mRNA
 A; Residues: 1-294 <HIF>
 A; Cross references: EMBL:X57839; PIDN:916218; PIDN:CAA40971.1; PID:916219
 R; Ferreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze, D.
 Plant Cell 3, 531-540, 1991
 A; Title: The *Arabidopsis* functional homolog of the p34cdc2 protein kinase.
 A; Reference number: JO0967; MUID:9300515
 A; Accession: JO0967
 A; Molecule type: mRNA
 A; Residues: 1-294 <FER>
 A; Cross references: GB:S45387; PIDN:9257373; PIDN:AAB23643.1; PID:9257374
 A; Experimental source: flower
 C; Comment: The protein is a key component of the eukaryotic cell cycle.
 C; Genetics:
 A; : cdc2
 A; : cdc2
 A; Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3
 C; Function:
 A; Description: phosphotransferase; protein kinase; required for G1 to S-phase transition
 C; Superfamily: kinase-related transforming protein; protein kinase homology
 C; Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F; 2-256/Domain: protein kinase homology <KIN>
 F; 10-18/Region: protein kinase ATP-binding motif
 F; 33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 10.1%; Score 68.5; DB 2; length 294;
 Best Local Similarity 36.2%; Pred No. 11;
 Matches 17; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 2 SEPWKPPSSRLTETLDPAEYN-ISPETRRAQAEERLAIRQLKRFY 47
 Db 240 AFPKWRPDTLETFVNLDPGVDLISKMLMDPTRRINAARALEHEY 286

Search completed: April 29, 2001, 06:45:36
 Job time: 307 sec



Qy	122	DRTFHLSY	129	AC	P48306;
Db	121	DRTFHLSY	128	DT	01-FEB-1996 (Rel. 33, Created)
RESULT	2	NBSM_BOVIN	STANDARD;	PRT;	128 AA.
ID		NBSM_BOVIN	STANDARD;	PRT;	128 AA.
AC		P48305;			
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT (EC 1.6.5.3)	(EC 1.6.5.3) (COMPLEX I-B15) (CT-B15) (HYPOTHETICAL PROTEIN WALTER)			
DE	(COMPLEX I-B15)	(CT-B15)			
GN	NDUBB4				
OS	BOS taurus (Bovine)				
OC	Mammalia; Metacosa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Odontognathidae; Bovinae; Bos.				
OC	Osteichthyes; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Odontognathidae; Bovinae; Bos.				
OC	Eukaryota; Metacosa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Odontognathidae; Bovinae; Bos.				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Ceti; Artiodactyla; Bovidae; Bos.				
OC	Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Ceti; Artiodactyla; Bovidae; Bos.				
OC	Eukaryota; Metacosa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Odontognathidae; Bovinae; Bos.				
OC	Eukaryota; Metacosa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Odontognathidae; Bovinae; Bos.				
RA	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	TISSUE=Heart;				
RX	MEDLINE=92389317; PubMed=1518044;				
RA	Walker J.E., Alzamendi J.M., Dupuis A., Fearnley I.M., Finel M., Medd S.M., Pilkington S.J., Rumsick M.J., Skehel J.M.;				
RT	"Sequences of 20 subunits of NADH:ubiquinone oxidoreductase from bovine heart mitochondria. Application of a novel strategy for sequencing proteins using the polymerase chain reaction."				
RT	J. Mol. Biol. 226(1):51-107(1992).				
RL	-1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN, THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE.				
CC	-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+)+ UBIQUINOL.				
CC	-1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.				
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE; MATRIX SIDE.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
DR	EMBL: X64198; CNA45107.1; -				
KW	Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Acetylation.				
FT	NIT-MET 0				
FT	MOD_RES 1 1 ACETYLATION MW: 15053 MN; CC1352E9B0DF7D5 CRC64;				
FT	SEQUENCE 128 AA; 15053 MW; ED762948C97B352 CRC64;				
Query Match	Best Local Similarity 75.1%; Score 509; DB 1; Length 128; Matches 94; Conservative 18; Mismatches 16; Indels 0; Gaps 0;				
Qy	2 SFPKYKPSLRLPTEDPAEYNISSETRRAQAERIAIRQLKREYLQYNDPNNRGLENPA 64				
Db	1 SFPKYKPSLRLPTEDPAEYNISSETRRAQAERIAIRQLKREYLQYNDPNNRGLENPA 64				
Qy	62 NPALLRIVARYARINVYFNRTPKNSLMGALCGRPLIFLYYIKTERRKELLIQKEKL 121				
Db	61 DPALVRIVARYARINVYFNRTPKNSLMGALCGRPLIFLYYIKTERRKELLIQKEKL 121				
Qy	122 DRTFHLSY 129				
Db	121 DRTFHLSY 128				
RESULT	4				
ID	GYRB_SYN3				
ID	GIRB_SYN3	STANDARD;	PRT;	1078 AA.	
AC	P77906;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DE	DNA GYrase SUBUNIT B (EC 5.99.1.3).				
GN	GYRB OR SLL2005.				
OS	Synechocystis sp. (strain PCC 6803).				
RESULT	3				
ID	NBSM_CHICK	STANDARD;	PRT;	133 AA.	

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TAXID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE97061201; PubMed=8905231;
 DE RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- FUNCTION: DNA GRASSE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
 CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
 CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
 CC DNA RINGS, INCLUDING CATEINNES AND KNOTTED RINGS.
 CC -!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
 CC OF DOUBLE-STRANDED DNA.
 CC -!- SUBUNITS: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
 CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
 CC ENZYME FORMS AN A2B2 TETRAMER.
 CC -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
 CC A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
 CC FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
 CC
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 CC
 DR EMBL: D90508; BAA17220.1; -.
 DR HSSP: P0682; IAJ6.
 DR InterPro: IPR000565; -.
 DR InterPro: IPR00124; -.
 DR InterPro: IPR00220; -.
 DR InterPro: IPR00228; -.
 DR pfam: PF00986; DNA_gyraseB_C; 1.
 DR pfam: PF00204; DNA_topoisoi; 2.
 DR PRINTS: PRO0418; TP12FAMILY.
 DR PROSITE: PS00117; TOPOISOMERASE_II; 1.
 DR PROSITE: PS00881; PROTEIN_SPLICING; FALSE_NEG.
 KR K竭 Isomerase; Topoisomerase; ATP-binding; Autocatalytic cleavage;
 KR Protein splicing.
 FT CHAIN 1 436 GYRB, 1ST PART (POTENTIAL).
 FT CHAIN 437 871 SSP_GYRB INNEIN (POTENTIAL).
 FT CHAIN 872 1078 GYRB, 2ND PART (POTENTIAL).
 FT SEQUENCE 1078 AA; 122819 MW; 6C02586DFE607B CRC64;
 SQ
 RESULT 6 Query Match
 Best Local Similarity 36.2%; Pred. No. 3.1;
 Matches 17; Conservative 6; Mismatches 18; Indels 6; Gaps 2;
 ID DNK3_SYN3
 ID DNK3_SYN3 STANDARD; PRT; 771 AA.
 AC P73098;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE DNAK PROTEIN 3 (HEAT SHOCK PROTEIN 70) (HSP70).
 GN DNK3 OR SLL1932.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TAXID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 DE RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";

RL DNA_Res_ 3:109-136(1996).
 CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
 CC -!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 CC
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 CC
 DR EMBL; D99903; BAA17123.1; -.
 DR HSSP; P10120; IATS; -.
 DR InterPro; IPR001023; -.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINS; PRO0001; HSP70; 1.
 DR PROSITE; PS00239; HSP70; 2; 1.
 DR PROSITE; PS00239; HSP70; 3; FALSE_NEG.
 DR Chaperone; ATP-binding; Multigene family; Heat shock; SEQUENCE; 771 AA; 86030 MW; BE715F28B3J2738C CRC64;
 CC
 Query Match 10.4%; Score 70.5; DB 1; Length 771; Best Local Similarity 30.5%; Pred. No. 12; Mismatches 9; Indels 15; Gaps 3; Matches 25; Conservative 9; Mismatches 33; Indels 15; Gaps 3; CC
 Qy 16 ETLDPAEYNSISPETRRAQERLAIRAQQLREYLQIYNPNRGLIENPALRWAYARTI- 74
 Db 570 EILDSEKDDERRLDQAQDILQDVLYELNRVRLQDD-KEEGFFE-----AIKKTF 621
 Qy 75 -----AVYPNFRPPKPKNSLMG 90
 Db 622 GDFDDDDYYNRPARDYNG 643
 CC
 RESULT 7 SX18_HUMAN STANDARD; PRT; 384 AA.
 ID SX18_HUMAN STANDARD; PRT; 384 AA.
 AC P35713; O938H8;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE TRANSCRIPTION FACTOR SOX-18.
 GN SOX18.
 OS *Akbariota*; *Metaooa*; *Chordata*; *Craniata*; *Vertebrata*; *Euteleostomi*; *OC*; *Mammalia*; *Eutheria*; *Primates*; *Catarrhini*; *Hominidae*; *Homo*.
 OC NCBI_TaxID:9606;
 RN [1]
 RP SUBSEQUENCE FROM N.A.
 RX PDB:1088556;
 RA Stanojcić S., Stevanović M.;
 RT "The human Sox18 gene: cDNA cloning and high resolution mapping.";
 RL *Biochim. Biophys. Acta* 1492:237-241(2000).
 RN [2]
 RP SUBSEQUENCE FROM N.A.
 RN TISSUE:Brain;
 RA Azuma T., Seki N., Yoshikawa T., Masuho Y., Muramatsu M.;
 RT "CDNA cloning, tissue expression and chromosome mapping of human homolog of SOX18";
 RT Submitted (OCT-1999) to the EMBL/GenBank/NCBI databases.
 RN [3]
 RP SUBSEQUENCE OF 96-149 FROM N.A.;
 RX MEDLINE=92310993; PubMed=1614875;
 RA Danny P., Swift S., Brand N., Bachade N., Barton P., Ashworth A.;
 RT "A conserved family of genes related to the testis determining gene, SRY.";
 RL Nucleic Acids Res. 20:2887-2887(1992).
 CC -!- FUNCTION: BINDS TO THE CONSENSUS SEQUENCE 5'-ACAAG-3' AND IS ABLE TO TRANS-ACTIVATE TRANSCRIPTION VIA THIS SITE (BY -CC

CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -!- SIMILARITY: CONTAINS 1 HMG BOX.
 CC -!- CAUTION: WAS CALLED SOX 8 BY REF. 3.
 CC
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 CC
 DR EMBL; AJ243898; CAB5835; 1; -.
 DR EMBL; AB033888; BAA17123.1; -.
 DR EMBL; X55654; CAA4615.1; -.
 DR PIR; S21482; S21482.
 DR PIR; S22941; S22941.
 DR HSSP; Q05056; IHRZ.
 DR MM; 601618; -.
 DR InterPro; IPR000910; -.
 DR Pfam; PF00055; HMG_box; 1.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein.
 FT DNA_BIND 85
 SQ SEQUENCE 384 AA; 40891 MW; 327462E519770062 CRC64;

CC
 Query Match 10.3%; Score 70; DB 1; Length 384; Best Local Similarity 20.8%; Pred. No. 6; Mismatches 21; Indels 43; Gaps 5; Matches 31; Conservative 21; Mismatches 43; Indels 54; Gaps 5; CC
 Qy 4 PRKYPPSIRTLPELDAEYNSISPETR-RQAERLAIR-----AOLKREYLQIYN 52
 Db 48-PASPPSPQRSPRSPPSPEPGYSPGSPAGRGERQADESRRPPNAMFWAKDERKLRAQON 107
 Qy 53 D-----+PNRGLIENPALRWAYARTIINVYPRPPKPKNSLMG 92
 Db 108 PDJHNAVLISKMLGKAWKELNAEKRPVEEARPLRVQLRDL---HPNYKYPR----- 157
 Qy 93 CGFGPLIFIYIYIKTTERURKEKLIQESKU 121
 Db 158 -----+RKKQQRKARRPLEPGIL 173
 CC
 RESULT 8 VATI_MEJJA STANDARD; PRT; 695 AA.
 ID VATI_MEJJA STANDARD; PRT; 695 AA.
 AC Q51675;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE V-type ATP synthase subunit I (EC 3.6.1.34) (V-type ATPase subunit I).
 GN ATP1 OR MJ0222.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus
 OC NCBI_TaxID:2190;
 RN [1]
 RP SUBSEQUENCE FROM N.A.
 RC STRAIN="JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96331999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Glodek A., Merrick J.M.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii,"
 RT Science 273:1058-1073(1996).
 CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON

CC GRADIENT ACROSS THE MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC
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 CC
 DR EMBL: U67478; AAB08208.1; -.
 DR TIGR: M0222; -.
 DR InterPro; IPR002490; -.
 DR Pfam; PF01496; V-ATPase_sub_a; 1.
 KW Hydrolase; Hydrogen ion transport; Transmembrane.
 FT TRANSMEM 392 412 POTENTIAL.
 FT TRANSMEM 425 445 POTENTIAL.
 FT TRANSMEM 497 517 POTENTIAL.
 FT TRANSMEM 534 554 POTENTIAL.
 FT TRANSMEM 556 576 POTENTIAL.
 FT TRANSMEM 605 625 POTENTIAL.
 FT SEQUENCE 695 AA: 76953 MW: F03E5CBE29D53D CRC64;
 SQ 13 TLPEPTLDPAEYNISPETRAQAEALAI-----RAQKREYLYQNPNNRGCLLENPA 64
 Db 217 TLKKEK---NVLESEIRKFREFERIDISVDEGTPSSEALSRSKIESELKATESERSNLIEKLK 272
 Qy 65 LLRKAVARYINVYINFPKPKNSLMGALCGFGPLIFIYIILKTERDRKEKKLIQECKLDRT 124
 Qy 1 ALAQWKEK-----ELLAVALSLSIKARGDAYSQFGKTDR 308
 Db 273 FHL 127
 Qy 125 FHL 127
 Db 309 YYI 311

RESULT 9
 CC21_ORYSA STANDARD: PRT: 294 AA.
 ID CC21_ORYSA STANDARD: PRT: 294 AA.
 AC P2618;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 1 (EC 2.7.1.-).
 GN CDC2.1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Ehrhartoideae; Oryzeae;
 OC Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NPIC1;
 RX MEDLINE=2293101; PubMed=1376401;
 RX Hasimoto J., Hirabayashi T., Hayano Y., Hata S., Ohashi Y.,
 RA Suzuki I., Usugi T., Toh E. A., Kikuchi Y.;
 RT "Isolation and characterization of cDNA clones encoding cdc2 homologues from Oryza sativa: a functional homologue and cognate variants";
 RT Mol. Gen. Genet. 233:10-16(1992).
 CC -!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
 CC -!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY SIMILARITY).

Query Match 10.3%; Score 70; DB 1; Length 695;
 Best Local Similarity 23.6%; Pred. No. 12; Mismatches 41; Indels 36; Gaps 3;
 Matches 29; Conservative 17; Mismatches 41; Indels 36; Gaps 3;

Qy 13 TLPEPTLDPAEYNISPETRAQAEALAI-----RAQKREYLYQNPNNRGCLLENPA 64
 Db 217 TLKKEK---NVLESEIRKFREFERIDISVDEGTPSSEALSRSKIESELKATESERSNLIEKLK 272
 Qy 65 LLRKAVARYINVYINFPKPKNSLMGALCGFGPLIFIYIILKTERDRKEKKLIQECKLDRT 124
 Db 273 FHL 127
 Qy 125 FHL 127
 Db 309 YYI 311

RESULT 10
 VPO_BHPI1 STANDARD: PRT: 298 AA.
 ID VPO_BHPI1 STANDARD: PRT: 298 AA.
 AC P51719;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE PROBABLE CAPSID SCAFFOLDING PROTEIN (ORF17).
 OS Bacteriophage HPI.
 OS Viruses; dsDNA viruses, no RNA stage; Tailed Phages; Myoviridae.
 OX NCBI_TaxID=10690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HPIC1;
 RX MEDLINE=9627973; PubMed=8710508;
 RX Esposito D., Fitzmaurice W. P., Benjamin R. C., Goodman S. D.,
 RA Waldman A. S., Scocca J. J.;
 RT "The complete nucleotide sequence of bacteriophage HPI DNA. ";
 RL Nucleic Acids Res. 24:2360-2368(1996).
 CC -!- SIMILARITY: STRONG, TO PHAGE P2 PROTEIN O.
 CC
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 CC
 DR EMBL: U24159; AAB09202.1; -.
 KW SEQUENCE 298 AA; 33702 MW; 6D2841468B700C1F CRC64;

Query Match 10.2%; Score 69; DB 1; Length 298;
 Best Local Similarity 26.9%; Pred. No. 5.7;
 Matches 39; Conservative 14; Mismatches 50; Indels 42; Gaps 8;

RE [1] MT UUMAN 11
 ID MTHR-HUMAN STANDARD PRT; 556 AA.
 AC P42858; Q9UQR2;
 DT 15-JUL-1995 (Rel. 32, Created)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20).
 GN MTHFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI-TaxID=9606;
 RN [1] SEQUENCE OF 1-415 FROM N.A., AND VARIANT GLN-157.
 RC TISSUE=LIVER;
 RX MEDLINE=95004587; PUBMED=7920641;
 RA Goeyette P., Sumner J.S., Milos R., Duncan A.M., Rosenblatt D.S.,
 RA Matthews R.G., Rozen R.;
 RT "Human methylenetetrahydrofolate reductase: isolation of cDNA,
 mapping and mutation identification.";
 RL Nat. Gener. 7:195-200(1994).
 RN [2] RP ERRATUM.
 RX MEDLINE=95038846; PUBMED=7951330;
 RA Goeyette P., Sumner J.S., Milos R., Duncan A.M., Rosenblatt D.S.,
 RA Matthews R.G., Rozen R.;
 RL Nat. Gener. 7:551-551(1994).
 RN [3] RP SEQUENCE FROM N.A.
 RA Rozen R., Goeyette P.;
 RT "cDNA for human methylenetetrahydrofolate reductase.";
 RL Patent number WO9533054, 07-DEC-1995.
 RN [4] SEQUENCE FROM N.A.
 RX MEDLINE=98345426; PUBMED=9680386;
 RA Goeyette P., Pai A., Milos R., Frosst P., Tran P., Chen Z., Chan M.,
 RA Rozen R.;
 RT "Gene structure of human and mouse methylenetetrahydrofolate reductase
 (MTHFR)." ;
 RL Mamm. Genome 9:652-656(1998).
 RN [5] SEQUENCE FROM N.A.
 RP Homburger A., Linnebank M., Winter C., Rapp B., Koch H.G.;
 RT "Revised translation initiation site of the human
 methylenetetrahydrofolate reductase (MTHFR).";
 RT Submitted (MAR 1999) to the EMBL/GenBank/DDBJ databases.
 RN [6] SEQUENCE FROM N.A.
 RP Variants Q-52; M-227; L-251; C-325; C-335; C-357, AND REVISION TO 177.
 RX MEDLINE=95243219; PubMed=772658;
 RA Goeyette P., Frost P., Rosenblatt D.S., Rozen R.;
 RT "Seven novel mutations in the methylenetetrahydrofolate reductase
 gene and genotype/phenotype correlations in severe
 methylenetetrahydrofolate reductase deficiency.";

RL Am. J. Hum. Genet. 56:1052-1059(1995).
 RN [7] RP . VARIANT VAL-222.
 RX MEDLINE=95375773; PubMed=7647779;
 RA Frost P., Blom H.J., Milos R., den Heijer M., Kluijtmans L.A.J.,
 RA van den Heuvel L.P., Rozen R.;
 RT "A candidate genetic risk factor for vascular disease: a common
 mutation in methylenetetrahydrofolate reductase.";
 RL Nat. Genet. 10:111-113(1995).
 RN [8] RP VARIANT PRO-51; PRO-323 AND CYS-377.
 RX MEDLINE=97094184; PubMed=8940272;
 RA Goeyette P., Christensen B., Rosenblatt D.S., Rozen R.;
 RT "Severe and mild mutations in cis of the methylenetetrahydrofolate
 reductase (MTHFR) gene, and description of five novel mutations in
 MTHFR.";
 RL Am. J. Hum. Genet. 59:1268-1275(1996).
 RN [9] RP VARIANT VAL-222.
 RX MEDLINE=98213590; PubMed=9545406;
 RA Schneider J.A., Rees D.C., Liu Y.-T., Clegg J.B.;
 RT "Worldwide distribution of a common methylenetetrahydrofolate
 reductase mutation.";
 RL Am. J. Hum. Genet. 62:1258-1260(1998).
 RN [10] RP VARIANT ALA-428.
 RX MEDLINE=98213566; PUBMED=9545395;
 RA van der Put N.N.J., Gabreëls F., Stevens E.M.B., Smeitink J.A.M.,
 RA Trijbels F.J.M., Eskes T.K.A.B., van den Heuvel L.P., Blom H.J.,
 RT "A second mutation in the methylenetetrahydrofolate reductase gene: an
 additional risk factor for neural-tube defects?";
 RL Am. J. Hum. Genet. 62:1044-1051(1998).
 RN [11] RP VARIANT SER-324 AND GLY-339.
 RX MEDLINE=98454315; PUBMED=9781030;
 RA Kluijtmans L.A.J., Wendel U., Stevens E.M.B., van den Heuvel L.P.W.J.,
 RA Trijbels F.J.M., Blom H.J.;
 RT "Identification of four novel mutations in severe
 methylenetetrahydrofolate reductase deficiency.";
 RL Eur. J. Hum. Genet. 6:257-265(1998).
 RN [12] RP VARIANT ALA-428.
 RX MEDLINE=98387934; PUBMED=9719624;
 RA Weisberg I., Tran P., Christensen B., Sibani S., Rozen R.;
 RT "A second genetic polymorphism in methylenetetrahydrofolate reductase
 (MTHFR) associated with decreased enzyme activity.";
 RL Mol. Genet. Metab. 64:159-172(1998).
 RN [13] RP VARIANT ASP-387; LEU-572 AND LYS-586.
 RX MEDLINE=20145670; PUBMED=10679944;
 RA Sibani S., Christensen B., O'Ferrall E., Saadi I., Hiou-Tim F.,
 RA Rosenblatt D.S., Rozen R.;
 RT "Characterization of six novel mutations in the
 methylenetetrahydrofolate reductase (MTHFR) gene in patients with
 homocystinuria";
 RL Hum. Mutat. 15:280-287(2000).
 CC -I- FUNCTION: CATALYZES THE CONVERSION OF 5,10-
 METHYLENETETRAHYDROFOLATE TO 5-METHYLTHIOTHYONINE.
 CC SUBSTRATE FOR HOMOCYSTEINE REMETHYLATION.
 CC -I- CATALYTIC ACTIVITY: 5-METHYLENETHYTHYONINE + NADP(+)=
 CC 5,10-METHYLENETETRAHYDROFOLATE + NADPH.
 CC -I- COFACTOR: FAD.
 CC -I- ENZYME REGULATION: ALLOSTERICALLY REGULATED BY S-
 CC ADENOSYLMETHIONINE.
 CC -I- PATHWAY: FOULATE METABOLISM.
 CC -I- SUBUNIT: HOMODIMER.
 CC -I- POLYMORPHISM: VARIANT VAL-222 IS A COMMON POLYMORPHISM WHICH HAS
 CC BEEN IMPLICATED IN THREE MULTIFACTORIAL DISEASES: OCCLUSIVE
 CC VASCULAR DISEASE, NEURAL TUBE DEFECTS (NTD) AND COLON CANCER.
 CC -I- DISEASE: DEFECTS IN MTHFR ARE THE CAUSE OF HOMOCYSTINEMIA
 CC (HOMOCYSTEINURIA II), AN AUTOSOMAL RECESSIVE DISEASE WHICH SHOWS A
 CC WIDE RANGE OF CLINICAL SYMPTOMS, SUCH AS DEVELOPMENTAL DELAY,

Db 790 SYEQYGPGENENLPT-DANRNFSSEDRQQCQECOLRREQQEQQEREVOLQLERREQER 847
 Qy 53 DPNRRGLIE-NPALLRWAYARTINWYPNFRP---TPKNSLMGALCGFGPLIFTYIYIK 105
 Db 848 EODERQDPGP-----EEPSVEEYSRALQENNAERDR-----YAEF 886
 Qy 107 TERDR--KERLIOEGKK 120
 Db 897 QERERQQETLQENQ 902

RESULT 13
 VIR6_OSCBR STANDARD; PRT; 1660 AA.
 AC 094637;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE KTELLOGENIN 6 PRECURSOR.
 GN PTR-6.
 OS Oscheius brevesophaga.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Rhabditinae; Oscheius.
 OX NCBI_TAXID=57871;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CWE1;

RX MEDLINE-96212989; PubMed=8676742;
 RA Winter C.E., Penha C., Blumenthal T.;
 RT "Comparison of a vitellogenin gene between two distantly related
 rhabditid nematode species.";
 RL Mol. Biol. Evol. 13:674-684(1996).
 CC -!- FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF
 NUTRIENTS DURING EMBRYONIC DEVELOPMENT (POTENTIAL).

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CC EMBL; U35419; ARB49749.1; -.
 DR HSSP; P11064; IPIR.
 DR InterPro; IPR001747; -.
 DR InterPro; IPR00186; -.
 DR InterPro; IPR01347; Vitellogenin_N; 1.
 DR fam; PF00094; vwd; 1.
 KW Storage protein; Multigene family; Signal.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 1650 VITELLOGENIN 6.
 FT CARBOHYD 237 237 N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CARBOHYD 383 383 N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CARBOHYD 695 695 N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CARBOHYD 1307 1307 N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CARBOHYD 1596 1596 N-LINKED (GlcNAc. . .) (POTENTIAL).
 FT CARBOHYD 1629 1629 N-LINKED (GlcNAc. . .) (POTENTIAL).
 SQ SEQUENCE 1660 AA; 192108 MW; 27782650678ABDD CRC64;

Query Match Similarity 10.2%; Score 69; DB 1; Length 1660;
 Best Local Similarity 24.8%; Pred. No. 43;
 Matches 34; Conservative 20; Mismatches 57; Index 26; Gaps 4;

Qy 6 YKPSSLRLDETLRPEYNISPETRRAQRAILRKQLRKYLYNDPNRGLLENPAL 65
 Db 631 YTWSLTKLTSSENAA---KEIRRVSOSLASIPVEOKYLESKHKTNWPNMGSAT 686
 Qy. 66 LWRAYARTINVYPNFRTPKNSLMGALCGFG-----PLIFY-----VIKTE 108
 Pb 687 LNWA---TIFSNDSVLPREITALETIVGEGEMWKYLQIGLYKUNLDSVLSKLQVE 741

RESULT 14
 CC2A_ARATH CC2A_ARATH STANDARD; PRT; 294 AA.
 ID CC2A_ARATH
 AC P24100;
 DT 01-MAR-1992 (Rel. 21, created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A (EC 2.7.1.-).
 GN CDC2A OR CDC2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93005715; PubMed=1840925;
 RA Ferreira P.C.G., Hemerly A.S., Villarroel R., van Montagu M., Inze D.;
 RT "The Arabidopsis functional homolog of the p34cdc2 protein kinase.";
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RX MEDLINE-92303027; PubMed=1937013;
 RA Hirayama T., Imajuku Y., Hirayama T., Matsui M., Oka A.;
 RT "Identification of two cell-cycle-controlling cdc2 genes homologs in
 Arabidopsis thaliana.";
 RL Gene 105:159-165(1991).
 CC [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-92316202; PubMed=1618302;
 RA Imajuku Y., Hirayama T., Endoh H., Oka A.;
 RT "Exon-intron organization of the Arabidopsis thaliana protein kinase
 genes CDC2a and CDC2b.";
 RL FEBS Lett. 304:73-77(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92319744; PubMed=1634002;
 RA Inze D., Ferreira P.C.G., Hemerly A.S., van Montagu M.;
 RT "Control of cell division in plants.";
 RL Biochem. Soc. Trans. 20:80-84(1992).
 CC -!- FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC
 CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES
 THE REPETITIVE CARBOXY-TERMINUS OF RNA POLYMERASE II.
 CC -!- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
 THE ENZYME, WHILE PHOSPHORYLATION AT THR-161 ACTIVATES IT (BY
 CC -!- SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC2/CDKX SUBFAMILY.

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 or send an email to license@isb-sib.ch).

CC DR EMBL; S45367; ARB23643.1; -.
 DR EMBL; M59198; AAA32831.1; -.
 DR EMBL; S45367; ARB23643.1; -.
 DR EMBL; M59198; AAA32831.1; -.
 DR EMBL; X57839; CRA04971.1; -.
 DR PIR; A48984; A48984.
 DR PIR; J00967; J00967.
 DR PIR; JQ1337; JQ1337.
 DR PIR; S23095; S23095.
 DR HSSP; P24941; IHCK.

Mon Apr 30 06:24:27 2001

us-09-726-899-3.rsp

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Gencore version 4.5

Om protein - protein search, using sw model

Run on: April 29, 2001, 06:45:39 ; Search time 19.67 Seconds
(without alignments)
768.674 Million cell updates/sec

Title: US-09-726-899-3

Perfect score: 678

Sequence: 1 MSFPKYKPPSSLRTLPETLDP..... DRKEKLQLQEGKLDRFFHLSY 129

Scoring table: BL0SUN62 Gapext 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

T number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 1.00%
Listing first 45 summaries

Database : SPTREMBL_15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	96.5	14.2	113	5 09V753
2	82	12.1	386	2 09L7P6
3	74.5	11.0	313	2 09K198
4	74	10.9	195	11 09WNB8
5	74	10.9	451	1 09V150
6	74	10.9	526	2 09WXH9
7	70.5	10.4	520	1 09LFZ1
8	70.5	10.4	585	10 09LG30
9	70.5	10.4	2067	5 09U30B
10	70	10.3	384	4 09NPB8
11	70	10.3	1025	5 025693
12	69.5	10.3	280	10 09XF46
13	69.5	10.3	280	10 09XF13
14	69	10.3	742	2 09ZB47
15	69.5	10.3	1276	13 09I18D1
16	69	10.2	679	4 09UQR2
17	69	10.2	759	4 09UGPB
18	69	10.2	760	4 095380
19	69	10.2	1026	5 09VLJ3

ALIGNMENTS

RESULT ID	PRELIMINARY;	PRT;	113 AA.
09V753	09V753; DT	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
09V753	AC	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
09V753	DE	DT	CG12859 PROTEIN
09V753	GN	DE	CG12859
09V753	OS	OS	Drosophila melanogaster (Fruit fly).
09V753	OC	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Drosophilidae; Drosophila.
09V753	OX	OX	NCBI_TaxID=7227;
09V753	RN	RN	[1]
09V753	RP	RP	SEQUENCE FROM N.A.
09V753	RC	RC	STRAT=BERKELEY;
09V753	RX	RX	MEDLINE=20196005; PubMed=10731132;
09V753	RA	RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallo R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Preffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borko D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodon K., Douc L.E., Downes M., Duan-Rocha D., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Galbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Koide C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purri V., Reese M.G.,
 RA Reinert K., Remington C., Saunders C.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E., Turner R., Venet J.C., Venter J.C., Wang A.H., Wang E., Wang X.,
 RA Svirska R., Tector C., Turner R., Venet E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA YE J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.-H., Zhong F.-N., zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE03813; AAF58210.1;
 DR FLYBASE; FBgn033951; CG12859;
 SQ SEQUENCE 113 AA; 13134 MW; 25A8CDB90F2DB414 CRC64;

Query Match 14.2%; Score 96.5; DB 5; Length 113;
 Local Similarity 29.3%; Pred. No. 0.01; Mismatches 27; Indels 9; Gaps 3;
 Matches 27; Conservative 20; Mismatches 36; Indels 9; Gaps 3;

Qy 42 QLKKEYLQYNDPPIRRL---GLIENPALLEWAVYRTINTIVPNPFTRPKISLMGAGCGFG 96
 :|:||:|:||:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 20 KLROEFLKGQSNPYPYRHATGEQGYVFDAGLARFOAMVRVSN-YEHFKPTGKSFRTGFLFAVVL 78

Qy 97 PLFIYIYIKTERREKLIQEKGK---DRTF 125
 :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 79 PIAIYAWAKAERDGCREEKYRTGQVAKDQF 110

RESULT 2

Q9LP6 PRELIMINARY; PRT; 386 AA.
 ID Q9LP6
 AC 09LP6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE PARC (FRAGMENT).
 GN PARC.
 OC Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OC NCBI_TAXID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM;
 RA Indler L.E., Jahan N.;
 RT Non-radioactive detection of ciprofloxacin resistance in *Yersinia*
 RT pestis.";
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF221695; AAF36389.1; -.
 FT NON_TER 386 386
 FT SEQUENCE 386 AA; 43477 MW; CC748E6024664CDD CRC64;

Query Match 12.1%; Score 82; DB 2; Length 386;
 Best Local Similarity 27.7%; Pred. No. 1.5; Mismatches 59; Indels 18; Gaps 5;
 Matches 36; Conservative 17; Mismatches 59; Indels 18; Gaps 5;

Qy 11 LRTLTPETLDPPEAYNISPETRRAQABER---LAIRAGLKRRELYQ----NDPNRGLI 60
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 252 LRDESDHENPTRLVIVPRTRNVDLDOQVMMSHLFATDLERSYRINMMIGLDNRPSVKLL 311

Qy 61 ENPALLRWAYAR-TINYVNPFRPPR--KNSLMGALCGCGPLFIYIYIKTERREK 114
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 312 E-ITTEWLVRQQTVRNLRNLFRKLRLHILEGULLIAFLNIDVHIRTTEDPKPL 369

Qy 115 LIQEGLKDRT 124
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 .Db 370 LMORFESSET 379

Query Match 10.9%; Score 74; DB 11; Length 195;
 Best Local Similarity 29.2%; Pred. No. 4.4;
 RT "Multiple gene products and sequences required for excision of the mobile element NBUL.;"
 RT Shoemaker N.B., Wang G.R., Salvers A.A.;
 RT Multiple gene products and sequences required for excision of the mobile element NBUL.;"
 RT mobilizable integrated Bacteroides element NBUL.;"
 RT J. Bacteriol. 182:928-936(2000).
 DR EMBL; AF238307; AAF74439.1;
 DR HYPOTHETICAL protein.
 SQ SEQUENCE 131 AA; 37128 MW; D1D4357FDB882D9 CRC64;

Query Match 11.0%; Score 74.5; DB 2; Length 313;
 Local Similarity 22.4%; Pred. No. 6.9; Mismatches 15; Indels 11; Gaps 3;
 Matches 15; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

Qy 4 PKYKPSSLRTLTETLDAEYNISPETRRAQARLAIRQLKEYLQYNDPHRRGLLENP 63
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 51 PYKEAARRRIGIDDRNP-DFF-----ELENVLLOSDABKIVNEFHTPKRSIV-P 99

Qy 64 AIRWAY 70
 ID Q9WUNB
 AC Q9WUNB;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE LADYBIRD-LIKE HOMEDOMAIN PROTEIN LBX2.
 GN LB2H OR LBX2.
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
 OC NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen F., Liu K.C., Epstein J.A.;
 RT "Lbx2, a novel murine homeobox gene related to the *Drosophila* ladybird brain.;"
 RT genes is expressed in the developing urogenital system, eye, and brain.;"
 RT Mech. Dev. 0-0-0(1999);
 RT DR EMBL; AF146150; AAD31905.1; -.
 DR HSSP; P23441; IFRIT.
 DR MGD-MGI-1342288; Lbx2h.
 DR INTERPRO; IPR00047; -.
 DR INTERPRO; IPR001556; -.
 DR PF0006; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTREPRESSR.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 SQ SEQUENCE 195 AA; 20916 MW; E106CE108933DE45 CRC64;

Matches	14;	Conservative	11;	Mismatches	17;	Indels	0;	Gaps
RT	Stanojcic S., Stevanovic M.;							
RT	The human SOX18 gene: cDNA cloning and high resolution mapping. ";							
RT	Biotech. Biophys. Acta 1492:237-241(2000);							
RP	[21]							
RP	SEQUENCE FROM N.A.							
RC	TISSUE=BRAIN;							
RA	Azuma T., Seki N., Yoshikawa T., Masuho Y., Muramatsu M.;							
RT	"cDNA cloning, tissue expression and chromosome mapping of human homolog of SOX18."							
RL	Submitted (OCT-1999) to the EMBL/GenBank/DDJB databases.							
RN	[3]							
RP	SEQUENCE FROM N.A.							
RC	TISSUE=BRAIN;							
RA	Dunn T.L., Myatt-Johnson L., Wright E.M., Hosking B.M., Koopman P.A.,							
RA	Muscat G.E.;							
RT	"Sequence and expression of sox-18 encoding a new HMG-box transcription factor.";							
RT	Gene 161:223-225(1995);							
RL	EMLB: AJ43896; CAB95835; 1; -							
DR	EMBL: AB033886; BAA94874; 1; -							
SO	SEQUENCE 384 AA; 40891 MW; 327462E51977062 CRC64;							
RESULT	12							
RP	09XF46	PRELIMINARY;	PRT;	280 AA.				
AC	Q9XF46;							
RP	09XF46; [1]							
DT	01-NOV-1999 (TREMBLEL 12, Created)							
DT	01-NOV-1999 (TREMBLEL 12, last sequence update)							
DT	01-OCT-2000 (TREMBLEL 15, last annotation update)							
DE	CELL DIVISION CONTROL PROTEIN 2 (FRAGMENT).							
OS	Phaseolus aureus (Mung bean) (Vigna radiata).							
OC	Eukaryote; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;							
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid I; Fabales; Fabaceae; Papilionoideae; vigna.							
OC	NCBI_TaxID=3916;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RA	Luo S., Liu S.-L., Wang Y., Liang H., Wang Y.-C., Han B.-W.;							
RT	"Cdc2 gene cloning and its expression along with differentiation of adventitious root in mung bean."							
RL	Submitted (FEB-1999) to the EMBL/GenBank/DDJB databases.							
DR	AF129886; AAD30506; 1; -							
DR	HSSP; P24941; 1HCL.							
DR	INTERPRO; IPRO00719; -							
DR	INTERPRO; IPRO01245; -							
DR	INTERPRO; IPRO02290; -							
PFAM; PF00069; pkinase; 1.								
DR	PRINTS; PR00109; TYRKINASE.							
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.							
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.							
KW	Cell division.							
FT	NON_TER	1	1					
SQ	SEQUENCE 280 AA; 32166 MW; 85826C20A864253E CRC64;							
RESULT	11							
RP	025693	PRELIMINARY;	PRT;	1025 AA.				
ID	Q25693;							
AC	Q25693; [1]							
DT	01-NOV-1996 (TREMBLEL 01, Created)							
DT	01-NOV-1996 (TREMBLEL 01, Last sequence update)							
DT	01-JUN-2000 (TREMBLEL 14, Last annotation update)							
DE	PFMDR2 PROTEIN.							
GN	PFMDR2							
OS	Plasmodium falciparum.							
OC	Jukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.							
OX	NCBI_TaxID=5833;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=D10;							
RX	MEDLINE=94333538; PubMed=7914495;							
RX	Rubio J.P., Compan A.F.;							
RT	"Plasmodium falciparum: the pfmdr2 protein is not overexpressed in chloroquine-resistant isolates of the malaria parasite."							
RT	Exp. Parasitol. 79:137-147(1994).							
RL	ATP-Binding; Transport;							
DR	EMBL: U04540; AAA21513.1; -							
DR	IINSPP; P13569; INBD.							
DR	INTERPRO; IPRO00140; -							
DR	INTERPRO; IPRO01617; -							
DR	PFAM; PF00005; ABC_tran; 1.							
DR	PFAM; PF00664; ABC_membrane; 1.							
DR	PROSITE; PS00211; ABC_TRANSPORTER; 1.							
KW	ATP-Binding; Transport;							
SO	SEQUENCE 1025 AA; 119152 MW; 91AF3BD8916D520D CRC64;							
Query Match	10.3%	Score	70	DB 5;	Length	1025;		
Best Local Similarity	33.3%	Pred.	No. 86;					

PRINTS: PRO0109; TYRKINASE.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR
 KW Cell division.
 FT NON_TER 1 1
 SEQUENCE 280 AA; 32166 MW; 85826C20A864253E CRC64;
 SQ
 Query Match 10.3%; Score 69.5; DB 10; Length 280;
 Best Local Similarity 34.0%; Pred. No. 20; Mismatches 16; Conservative 12; MisMatches 18; Indels 1; Gaps 1;
 Matches 16; Conservative 12; MisMatches 18; Indels 1; Gaps 1;
 QY 2 SFPKYKPSSLRPLPTEIDPAEYN-ISPETRRAQEAERLAIRAQQLREY 47
 DB 230 AFPKWQPKDLKIVVVPNLDPAGLDLSRMLHLDPSKRITCRSALEHEY 276
 RESULT 14
 ID 0927
 AC QZB47
 DT 29ZB47; 01-MAY-1999 (TREMBlrel. 10, Created)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DR EMBL; U49397; AAC07148.1;
 GN CPA.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS101;
 RA Podbielski A., Wochnik M., Leonard B.A.B., Schmidt K.H.;
 RT "Characterization of nra, a global negative regulator gene in group A
 streptococci.";
 RL Mol. Microbiol.; 31:0-0(1999).
 DR NCBI_TAXID=1314;
 SQ 83682 MW; 97A1FF44B4ECB944 CRC64;
 Query Match 10.3%; Score 69.5; DB 2; Length 742;
 Best Local Similarity 24.8%; Pred. No. 65; Mismatches 27; Conservative 17; MisMatches 44; Indels 21; Gaps 5;
 Matches 27; Conservative 17; MisMatches 44; Indels 21; Gaps 5;
 QY 8 PSSLRLPTEIDPAEYN-ISPETRRAQEAERLAIRAQQLREY 67
 DB 319 PNGTYLTETSSPCKYI-----AEPIKFRVENKKVFLVKQGSQ---VENPN-KE 365
 QY 68 WATPATINTVNPNEPTPKNSLGMALCCGGFLIFTYVTKPERDRKRLI 116
 DB 366 VAEDPSVEAYNDFMDEE-----VLSGFTPYGKFYI-ATNKDKSSQV 406
 RESULT 15
 Q9IBD1
 ID Q9TB1
 AC Q9IBD1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE MYOSEN VI.
 GN CM6.
 OS Gallus gallus (Chicken); Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
 OC Archosauria; Aves; Neognathae; Galliformes;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kendrick Jones J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
 [2]

Mon Apr 30, 06:24:27 2001

us-09-726-899-3.rspt



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 29, 2001, 06:34:44 ; Search time 20.28 Seconds
 (without alignments)
 363.612 Million cell updates/sec

Title: US-09-726-899-3
 Perfect score: 678
 Sequence: I MSFPKIKKPSSLRTLPTLDP.....DRKEKLHQEGKLDRTFHLSY 129

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 390729 seqs, 57163235 residues

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_0401:*

1: /SID56/gcdata/geneseq/geneseq/AAI1980.DAT: *
 2: /SID56/gcdata/geneseq/geneseq/AAI1981.DAT: *
 3: /SID56/gcdata/geneseq/geneseq/AAI1982.DAT: *
 4: /SID56/gcdata/geneseq/geneseq/AAI1983.DAT: *
 5: /SID56/gcdata/geneseq/geneseq/AAI1984.DAT: *
 6: /SID56/gcdata/geneseq/geneseq/AAI1985.DAT: *
 7: /SID56/gcdata/geneseq/geneseq/AAI1986.DAT: *
 8: /SID56/gcdata/geneseq/geneseq/AAI1987.DAT: *
 9: /SID56/gcdata/geneseq/geneseq/AAI1988.DAT: *
 10: /SID56/gcdata/geneseq/geneseq/AAI1989.DAT: *
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 13: /SID56/gcdata/geneseq/geneseq/AAI1993.DAT: *
 14: /SID56/gcdata/geneseq/geneseq/AAI1994.DAT: *
 15: /SID56/gcdata/geneseq/geneseq/AAI1995.DAT: *
 16: /SID56/gcdata/geneseq/geneseq/AAI1996.DAT: *
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 19: /SID56/gcdata/geneseq/geneseq/AAI1999.DAT: *
 20: /SID56/gcdata/geneseq/geneseq/AAI2000.DAT: *
 21: /SID56/gcdata/geneseq/geneseq/AAI2001.DAT: *
 22: /SID56/gcdata/geneseq/geneseq/AAI2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
1	678	100.0	129	19 W69225	NADH dehydrogenase
2	503	74.2	113	20 Y76629	Human ovarian tumor
3	76	11.2	16	21 B53504	Human colon cancer
4	72	10.6	290	21 G33365	zea mays protein f
5	69.5	10.3	292	21 B35797	protein involved in
6	69.5	10.3	294	20 W95690	oryza sativa Cdc2
7	69	10.2	656	17 R88358	Human methyl-ene- te
8	69	10.2	660	17 R88359	Human methyl-ene- te
9	69	10.2	660	21 Y96186	Human methyl-eneter
10	68.5	10.1	204	21 G54044	Arabidopsis thaliana
11	68.5	10.1	237	21 G11215	Arabidopsis thaliana
SUMMARIES					
RESULT 1					
W69225				ID W69225	standard; Protein: 129 AA.
AC				XX	
W69225;				XX	
DT				XX	
18-FEB-1999				XX	(first entry)
DE				XX	
NADH dehydrogenase subunit NDS-2.				XX	
XK				XX	
NADH dehydrogenase subunit; sympathetic nervous system disease; myopathy; KW				XX	
KW				XX	nicotinamide-adenine dinucleotide dehydrogenase; cancer; leukaemia;
KW				XX	immune system disorder; neurodegenerative disease; therapy; NDS-2.
OS				XX	
Homo sapiens.				XX	
XX				XX	
PN				XX	W09831815-A2.
XX				XX	
PD				XX	23-JUL-1998.
XX				XX	
PF				XX	17-DEC-1997; 97WO-US23970.
XX				XX	
PR				XX	17-JAN-1997; 97US-0785065.
XX				XX	
PA				XX	(INCY-) INCYTE PHARM INC.
PI				XX	Bandman O, Goli SK, Hillman JL;
PI				XX	
WPI: 1998-414112/35.				XX	
DR				XX	N-PSDB; V44787.
PT				XX	Human nicotinamide-adenine di:nucleotide dehydrogenase sub-units - useful for, e.g. diagnosis, treatment and prevention of cancer, myopathy, immune system disease and neuro:degeneration

XX
PS Claim 19; Fig 2; 80pp; English.

DR

N-PSDB;

277502.

XX This sequence represents the NADH (reduced nicotinamide-adenine dinucleotide) dehydrogenase subunit, NDS-2, of the invention. Cells containing the DNA are used to produce the recombinant subunits. Antagonists of NDS-1 (typically antisense sequences or ribozymes) are used to treat or prevent cancer (leukaemia and solid cancers) and immune system disorders (e.g. asthma, diabetes, rheumatoid arthritis, osteoporosis and many others); NDS-2 and NDS-4 are used to treat myopathy (e.g. ophthalmoplegia, myoclonic epilepsy and lactic acidosis), while their antagonists are used to treat cancer and disease of the sympathetic nervous system (e.g. hypertension, arrhythmia and migraine); NDS-3 is also used to treat myopathy and its antagonists to treat cancer and neurodegenerative disease (e.g. Alzheimer's, Huntington's and Parkinson's diseases, epilepsy and Down's syndrome). In all cases NDS or their antagonists may be expressed from gene therapy vectors. AB may be used therapeutically as antagonist; as immunosassa reagent for diagnosis or monitoring such diseases; in competitive screening assays for agents that bind specifically to the subunits, and for affinity purification of the subunits from natural sources. The DNAs are useful as primers and probes for diagnosis and monitoring (including detecting predisposition to cancer); for gene mapping or identifying related sequences, while the subunits are also used to raise antibodies and to screen for specific binding agents.

CC Sequence 129 AA;

Query Match Best local Similarity 100.0%; Score 678; DB 19; Length 129;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFFKPKYKPSLRLTFLTPAENISPERTRRADERLAIRALRAQLREYLQYNDPNRRLGI 60
Db 1 msfkpkypskirptptlqpaeynisperrraderlairlraqreyllqyndpnrrgl 60
QY 61 ENPALLRWAYARTINVYPNFRPTPKNSLMGALCGFPLIFIYIKTERDRKEKLQEGK 120
Db 61 enpallrwayartinvypnfrptpknslmgalcgfpplifiyyikterdrkeklqegk 120
QY 121 LDRTFFHLSY 129
Db 121 ldrtffhlsy 129

RESULT 2

IT 76629 standard; Protein; 113 AA.

AC Y76629;

XX 10-APR-2000 (first entry)

XX Human ovarian tumor EST fragment encoded protein 125.
DE Human ovarian tumor EST fragment encoded protein 125.

XX Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment.

XX Homo sapiens.

XX DE19817557-A1.

XX PN

XX PD 21-OCT-1999.

XX 09-APR-1998; 98DE-1017557.

XX 09-APR-1998; 98DE-1017557.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX PI Rosenthal A, Specht T, Hinmann B, Schmitt A, Pilarsky C, Dahl E;

Sequence 113 AA;

Query Match Best Local Similarity 99.0%; Score 503; DB 20; Length 113;
Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 34 AERLAIRAQKREYLQYNDPNRGLIENPALLRWAYARTINVYPNFRPTPKNSLMGALC 93
Db 18 serlairaqkreyllqyndpnrrgliepalrlwayartinvypnfrptpknslmalc 77
QY 94 GFGPLIFIYIKTERDRKEKLQEGKLDRTHLSY 129
Db 78 fgplifiyyikterdrkeklqegkldrtfhlsy 113

RESULT 3

IT B53504 standard; Protein; 16 AA.

AC B53504;

XX DT 09-MAR-2001 (first entry)

XX Human colon cancer antigen protein sequence SEQ ID NO:1044.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnery; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotoxic; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; Homo sapiens. OS Homo sapiens.

XX PN WO200055351-A1.

XX 21-SEP-2000.

XX PR 08-MAR-2000; 2000WO-US05883.

XX 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.

WPI; 1999-591920/51.

N-PSDB;

277502.

New nucleic acid sequences expressed in ovarian and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents

XX Claim 25; Page 295; 310pp; German.

DR

N-PSDB;

277502.

This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of the expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of fragments encoded by the human ovarian tumor cDNA library derived EST fragments represented in Z77450-277572.

Sequence 113 AA;

PR	XX	Rosen CA, Ruben SM;
PR	XX	WPI; 2000-587534/55.
DR	XX	N-PSDB; C9861.
PT	Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer	
PT	XX	Claim 11; Page 1624; 2104pp; English.
PS	XX	c9791 to c98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in B5324 to B5406. The human colon cancer antigens can have cyostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, pulmonary, nephrotoxic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. C98764 to c98772 and B54007 represent sequences used in the exemplification of the present invention.
SQ	XX	Sequence 16 AA;
RESULT	4	Query Match
ID	G33365	Best local Similarity 93.8%; Score 76; DB 21; Length 16; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	114 KLIQEKGKLDRTFELSY 129	Db 1 kilqvkgkldrtfhsly 16
XX	XX	18-OCT-2000 (first entry)
DT	XX	DT
DR	XX	DR
KW	XX	KW
KW	XX	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
OS	XX	zea mays subsp. mays.
XX	EP1033405-A2.	XX
PD	XX	06-SEP-2000.
PF	XX	25-FEB-2000; 2000EP-0301439.
PR	XX	25-FEB-1999; 990US-0121825.
PR	XX	05-MAR-1999; 990US-01223180.
PR	XX	09-MAR-1999; 990US-0123548.
PR	XX	23-MAR-1999; 990US-0125788.
PR	XX	25-MAR-1999; 990US-0126264.
PR	XX	29-MAR-1999; 990US-0126785.
PR	XX	01-APR-1999; 990US-0127462.
PR	XX	06-APR-1999; 990US-0128234.
PR	XX	08-APR-1999; 990US-0128714.
PR	XX	16-APR-1999; 990US-0129845.
PR	XX	19-APR-1999; 990US-0130077.
PR	XX	21-APR-1999; 990US-0130449.
PR	XX	23-APR-1999; 990US-0130510.
PR	XX	28-APR-1999; 990US-0131449.
PR	XX	30-APR-1999; 990US-0132048.
PR	XX	04-MAY-1999; 990US-0132484.
PR	XX	05-MAY-1999; 990US-0132485.
PR	XX	06-MAY-1999; 990US-0132486.
PR	XX	07-MAY-1999; 990US-0132487.
PR	XX	11-MAY-1999; 990US-0132486.
PR	XX	14-MAY-1999; 990US-0134218.
PR	XX	14-MAY-1999; 990US-0134219.
PR	XX	14-MAY-1999; 990US-0134340.
PR	XX	18-MAY-1999; 990US-0134768.
PR	XX	19-MAY-1999; 990US-0134941.
PR	XX	20-MAY-1999; 990US-013514.
PR	XX	21-MAY-1999; 990US-013533.
PR	XX	24-MAY-1999; 990US-0135629.
PR	XX	25-MAY-1999; 990US-0136021.
PR	XX	27-MAY-1999; 990US-0136392.
PR	XX	28-MAY-1999; 990US-0136782.
PR	XX	01-JUN-1999; 990US-013722.
PR	XX	03-JUN-1999; 990US-0137528.
PR	XX	04-JUN-1999; 990US-013774.
PR	XX	07-JUN-1999; 990US-013774.
PR	XX	08-JUN-1999; 990US-0138094.
PR	XX	10-JUN-1999; 990US-013847.
PR	XX	14-JUN-1999; 990US-0139119.
PR	XX	16-JUN-1999; 990US-0139452.
PR	XX	16-JUN-1999; 990US-0139453.
PR	XX	17-JUN-1999; 990US-0139492.
PR	XX	18-JUN-1999; 990US-0139454.
PR	XX	18-JUN-1999; 990US-0139455.
PR	XX	18-JUN-1999; 990US-0139456.
PR	XX	18-JUN-1999; 990US-0139457.
PR	XX	18-JUN-1999; 990US-0139458.
PR	XX	18-JUN-1999; 990US-0139459.
PR	XX	18-JUN-1999; 990US-0139460.
PR	XX	18-JUN-1999; 990US-0139461.
PR	XX	18-JUN-1999; 990US-0139462.
PR	XX	18-JUN-1999; 990US-0139463.
PR	XX	18-JUN-1999; 990US-0139750.
PR	XX	18-JUN-1999; 990US-0139763.
PR	XX	21-JUN-1999; 990US-0139817.
PR	XX	22-JUN-1999; 990US-0139890.
PR	XX	23-JUN-1999; 990US-0140353.
PR	XX	24-JUN-1999; 990US-0140693.
PR	XX	28-JUN-1999; 990US-0140823.
PR	XX	29-JUN-1999; 990US-0140981.
PR	XX	30-JUN-1999; 990US-0141287.
PR	XX	01-JUL-1999; 990US-0141842.
PR	XX	01-JUL-1999; 990US-0142154.
PR	XX	02-JUL-1999; 990US-0142055.
PR	XX	06-JUL-1999; 990US-0142390.
PR	XX	08-JUL-1999; 990US-0142803.
PR	XX	09-JUL-1999; 990US-0142920.
PR	XX	12-JUL-1999; 990US-0142977.
PR	XX	13-JUL-1999; 990US-0143542.
PR	XX	14-JUL-1999; 990US-0143624.
PR	XX	15-JUL-1999; 990US-0144005.
PR	XX	16-JUL-1999; 990US-0144086.
PR	XX	16-JUL-1999; 990US-0144086.
PR	XX	19-JUL-1999; 990US-0144325.
PR	XX	19-JUL-1999; 990US-0144331.
PR	XX	19-JUL-1999; 990US-0144333.
PR	XX	19-JUL-1999; 990US-0144334.
PR	XX	19-JUL-1999; 990US-0144335.

PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-014632.
 PR 20-JUL-1999; 99US-014884.
 PR 21-JUL-1999; 99US-014814.
 PR 21-JUL-1999; 99US-015086.
 PR 21-JUL-1999; 99US-015088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 06-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 09-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 10-AUG-1999; 99US-0147935.
 PR 11-AUG-1999; 99US-0148171.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 16-AUG-1999; 99US-0148684.
 PR 17-AUG-1999; 99US-0149368.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 23-AUG-1999; 99US-0149929.
 PR 25-AUG-1999; 99US-0149930.
 PR 26-AUG-1999; 99US-0150566.
 PR 27-AUG-1999; 99US-0151065.
 PR 30-AUG-1999; 99US-0151080.
 PR 31-AUG-1999; 99US-0151303.
 PR 01-SEP-1999; 99US-0151930.
 PR 10-SEP-1999; 99US-0152363.
 PR 13-SEP-1999; 99US-0153070.
 PR 15-SEP-1999; 99US-0153758.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-015139.
 PR 23-SEP-1999; 99US-015486.
 PR 24-SEP-1999; 99US-0156659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
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 PR 14-OCT-1999; 99US-0159329.
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 PR 14-OCT-1999; 99US-0159637.
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 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
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 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 10.6%; Score 72; DB 21; Length 290;
 Best Local Similarity 26.0%; Pred. No. 1.9; Matches 32; Conservative 32; Mismatches 15; Indels 32; Gaps 6;

Qy	4	PYKVPPSLRTPEPTLPAEYNNSPERRQAERLAIRAOQLKREYLLQYN--DPNR--	5
Db	10	Dlfcppplvarp--pa--ssppagrpasqtlavrarekldamfgyrkadpleeggs	63
Qy	58	--GLENPALLRAYARTINNVPNFR--	-PPKNSLMGALCGFGPL 98
Db	64	sllypgmtstesr-lrwafvkrklyivltvglamtaavsafrvvkypavsnffivsagliy	122

Qy 99 IFI 101
 Db 123 ifl 125

RESULT 5

B35797 ID B35797 standard; Protein: 292 AA.
 XX AC B35797;
 XX DT 23-FEB-2001 (first entry)
 XX DE Protein involved in cell cycle regulation SEQ ID 14.
 XX KW Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
 KW cotton; rice; barley; millet.
 XX OS Zea mays.
 XX PN WO2006040-A2.
 XX PD 02-NOV-2000.
 XX PF 13-APR-2000; 2000WO-US09975.
 XX PR 22-APR-1999; 99US-0130849.
 XX PA (PION-) PIONER HT-BRED INT INC.
 XX PT Heilentjaris TG, Habben JE, Sun Y;
 XX DR WPI; 2000-68733/67.
 DR N-PSDB; C83104.
 XX PT Nucleic acids useful for producing transgenic plants, preferably maize,

PT with increased cell cycle gene activity, preferably activity of cyclin
 PT and/or cyclin-dependent kinase.
 XX
 PS Claim 16; Page 93-94; 122pp; English.

CC Polynucleotide sequences C83101 - C83113 encode proteins B35794 - B35806 which are involved in regulating the cell cycle. The protein and DNA sequences have been isolated from Zea mays (corn), and the invention also includes oligonucleotides C83114 - C83139 which are related to the cell cycle polynucleotides. The cell cycle polynucleotide sequences are useful for producing transgenic plants such as maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet with increased levels of cell cycle gene activity, such as activity of cyclin and cyclin-dependent kinases. The DNA sequences are also useful as probes for detecting deficiencies in the level of mRNA in screening for desired transgenic plants, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting any number of allelic variants, orthologs or paralogs of the gene, and site-directed mutagenesis in eukaryotic cells. The DNA sequences are also useful for recombinant expression of the encoded polypeptides and as immunogens for preparing and screening antibodies. A transgenic plant comprising an expression cassette including a cell cycle regulatory gene is useful for assaying enzyme agonists and antagonists, and as immunogens or antigens to obtain antibodies. The antibodies are useful in assaying expression levels of cell cycle regulatory proteins, for identifying and isolating nucleic acids from expression libraries, for identifying homologues of polypeptides from other species, and for purification of the proteins.

XX Sequence 292 AA;

Query Match 10.3%; Score 69.5; DB 21; Length 292;
 Best Local Similarity 34.0%; Pred. No. 3.9; Mismatches 18; Indels 1; Gaps 1;
 Matches 16; Conservative 12; MisMatch 18; Indels 1; Gaps 1;
 CC W95690;
 AC W95690;
 XX DT 08-JUN-1999 (first entry)
 XX Oryza sativa Cd2 protein kinase.
 XX cdc2; protein kinase; diagnosis; infection; immunosuppression;
 KW AIDS; acquired immunodeficiency syndrome; diagnosis; therapy;
 KW organ transplantation.
 OS Oryza sativa.
 XX PN W09856799-A1.
 XX PD 17-DEC-1998.
 XX PF 12-JUN-1998; 98WO-US12100.
 XX PR 13-JUN-1997; 97US-0874347.
 XX PA (MAYO-) MAYO FOUNDATION.
 XX PI Gustafson MP, Leof EB, Limper AH, Thomas CF;
 XX DR WPI; 1999-080877-07.
 XX PT New isolated polynucleotide encoding a Pneumocystis carinii cdc2 polypeptide - useful for diagnosing or monitoring P. carinii

PT infection in patients with chronic immunosuppression
 XX Example; Pages 44-45; 67pp; English.

CC The sequence is that of a Cdc2 polypeptide.
 CC The Cdc2 polypeptides are useful in treating P. carinii pneumonia in patients with chronic immunosuppression. Conditions associated with P. carinii include acquired immune deficiency syndrome (AIDS), solid tumors, hematological malignancies, organ transplantation, and inflammatory conditions. The polypeptides are additionally useful in identifying agents that inhibit the phosphorylation activity of P. carinii Cdc2 polypeptides. The polypeptide and its antibodies are useful for diagnosing or monitoring P. carinii infection in patients. The P. carinii Cdc2 polypeptides allow a therapeutic approach to treating P. carinii pneumonia because they are not limited by significant side effects. Polynucleotides encoding P. carinii Cdc2 enable in vitro production of the protein, which can be used in studying the organism (especially its life cycle) and developing new therapies.

XX Sequence 294 AA;

Query Match 10.3%; Score 69.5; DB 20; Length 294;
 Best Local Similarity 36.2%; Pred. No. 3.9; Mismatches 20; Indels 1; Gaps 1;
 Matches 17; Conservative 9; MisMatch 20; Indels 1; Gaps 1;
 CC R88358;
 AC R88358;
 XX DT 15-OCT-1995 (first entry)
 XX DE Human methylene-tetrahydrofolate-reductase.
 XX KW Methylenetetrahydrofolate-reductase; MTHFR; gene therapy; cardiovascular disease; neurological disease; folic acid metabolism; EC-1.5.1.20; enzyme.
 XX OS Homo sapiens.
 XX PN W09533054-A1.
 XX PD 07-DEC-1995.
 XX PF 25-MAY-1995; 95WO-CA00314.
 XX PR 26-MAY-1994; 94GB-0010620.
 XX PR (UWMC-) UNIV MCGILL.
 XX PI Goyette P, Rozen R;
 XX DR WPI; 1996-030565/03.
 XX DR N-P5DB; T09689.
 XX PT Human methylene-tetrahydrofolate reductase cDNA probe - for detection of sequence abnormalities in methylene-tetrahydrofolate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders.
 XX Disclosure; Fig. 6A-6C; 66pp; English.

CC This is the protein sequence encoding human MTHFR, the gene of which has been localised to chromosome 1p36.3. Deficiencies of this protein may lead to cardiovascular and neurological disorders and disorders influences by folic acid metabolism.

SQ	Sequence	656 AA:	Db	504 wqpsggvfvkaylefftsretaearllqvikkylervnyhl 544
Query Match	10.2%; Score 69; DB 17; Length 656;		RESULT	9
Best Local Similarity	28.7%; Pred. No. 13; Mismatches 32; Indels 26; Gaps 6;		Y96186	standard; Protein; 660 AA.
Matches	29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;		ID	Y96186 standard; Protein; 660 AA.
Qy	35 ERLAIAQKLYLQNDPNNRGLLENPALLRWAVARTINVPNFRPTKNSLNGALCG 94		XX	
Db	458 eplaeatslikeelrv--nrgil-----tinsqphngkpsd--pivg 499		AC	Y96186;
Qy	95 FGP--LIF--IYVLIKTERDRKEKLIQ--EGKIDRTRFL 127		DT	19-DEC-2000 (first entry)
Db	500 wqpsggvfvkaylefftsretaearllqvikkylervnyhl 540		XX	
RESULT	8		DE	Human methylenetetrahydrofolate reductase.
R88359			XX	
XX	R88359 standard; Protein; 660 AA.		Methylenetetrahydrofolate reductase; MTHFR; human; folic acid;	
AC			KW	cardiovascular disorder; cancer; neuroblastoma;
XX	R88359;		KW	colorectal carcinoma; osteoporosis; neural tube defect;
DT	15-OCT-1995 (first entry)		KW	neurological disorder; gene therapy; diagnosis.
XX	Human methylene-tetrahydrofolate-reductase cDNA.		XX	
XX			OS	Homo sapiens.
XX			XX	
KW	Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy;		PR	W0200052205-A2.
KW	cardiovascular disease; neurological disease; folic acid metabolism;		XX	
KW	EC-1.5.1.20; enzyme.		PA	(UYMC-) UNIV MCGILL.
XX			PD	08-SEP-2000.
OS	Homo sapiens.		XX	
XX			PF	28-FEB-2000; 2000WO-1B00442.
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XX			PR	01-MAR-1999; 99US-0258928.
XX			XX	
XX			PA	PR
PD	07-DEC-1995.		XX	
XX			PI	Roen R, Goyette P;
XX			XX	
PF	25-MAY-1995; 95NO-CA00314.		PR	WPI; 2000-572192/53.
XX			XX	
XX	26-MAY-1994; 94GB-0010620.		DR	N-PSDB; A50633, A50634.
XX			XX	
PR	(UYMC-) UNIV MCGILL.		PT	cDNA probe for the human methylenetetrahydrofolate reductase (MTHFR),
PR	Goyette P, Rozen R;		PT	useful in gene therapy and for diagnosing or treating MTHFR deficiency
PR	WPI; 1996-030565/03.		PT	which is associated with cardiovascular disorders or cancer
PR	N-PSDB; T09694.		XX	
PA			PS	Claim 1; FIG 1A-F; 93PP; English.
PA			XX	
PA			CC	The present sequence is that of human methylenetetrahydrofolate
PA			CC	reductase (MTHFR), an enzyme catalysing the NADPH-linked reduction
PA			CC	of 5,10-methylene-tetrahydrofolate to 5-methyltetrahydrofolate, a
PA			CC	co-substrate for methylation of homocysteine to methionine. A cDNA
PA			CC	probe for human MTHFR is claimed. This probe can be used to
PA			CC	identify MTHFR sequence abnormalities in individuals with severe or
PA			CC	mild MTHFR deficiency. MTHFR deficiency may be associated with
PA			CC	a cardiovascular disorder, cancer (especially neuroblastoma or
PA			CC	colorectal carcinoma), osteopetrosis, neural tube defect. In an
PA			CC	offspring of a patient, neurological disorders, and other disorders
PA			CC	influenced by folic acid metabolism. Also claimed are methods for
PA			CC	treating MTHFR deficiency by gene therapy or by administration of
PA			CC	MTHFR protein. Cancer can be treated by inhibiting MTHFR gene
PA			CC	expression or MTHFR protein activity, or by administering an agent
PA			XX	that modifies MTHFR gene expression.
PA			SQ	Sequence 660 AA;
Query Match	10.2%; Score 69; DB 21; Length 660;		Query Match	10.2%; Score 69; DB 21; Length 660;
Best Local Similarity	28.7%; Pred. No. 13; Mismatches 32; Indels 26; Gaps 6;		Best Local Similarity	28.7%; Pred. No. 13; Mismatches 32; Indels 26; Gaps 6;
Matches	29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;		Matches	29; Conservative 14; Mismatches 32; Indels 26; Gaps 6;
Qy	35 ERLAIAQKLYLQNDPNNRGLLENPALLRWAVARTINVPNFRPTKNSLNGALCG 94		Qy	35 ERLAIAQKLYLQNDPNNRGLLENPALLRWAVARTINVPNFRPTKNSLNGALCG 94
Db	462 eplaeatslikeelrv--nrgil-----tinsqphngkpsd--pivg 503		Db	462 eplaeatslikeelrv--nrgil-----tinsqphngkpsd--pivg 503
Qy	95 FGP--LIF--IYVLIKTERDRKEKLIQ--EGKIDRTRFL 127		Qy	95 FGP--LIF--IYVLIKTERDRKEKLIQ--EGKIDRTRFL 127
Db	504 wqpsggvfvkaylefftsretaearllqvikkylervnyhl 544		Db	504 wqpsggvfvkaylefftsretaearllqvikkylervnyhl 544

RESULT	10	
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ID	G54044 standard; Protein; 204 AA.	
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AC	G54044;	
XX		
DT	18-OCT-2000 (first entry)	
XX		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 68865.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
KW	Arabidopsis thaliana.	
OS		
XX		
PN	EP103405-A2.	
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PD	06-SEP-2000.	
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PR	05-FEB-2000; 2000EP-0301439.	
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PR	25-FEB-1999; 99US-0121825.	
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PR	25-MAR-1999; 99US-0126264.	
PR	29-MAR-1999; 99US-0126785.	
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PR	08-APR-1999; 99US-0128714.	
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Query Match 10.1%; Score 68.5%; DB 21; Length 237;
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QY	2 SEPKVKPSSRLTPETLDAEYN - SPETRRAQARLAQLKREY 47
Db	183 atpkwkptdlettfvbnldpdgvdllskmlmmpdkrinaraalehey 229

RESULT 12

G54043	ID G54043 standard; Protein: 237 AA.
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AC	G54043;
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D	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 68864.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.

OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
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 PR 25-FEB-2000; 2000EP-0301439.
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GenCore version 4.5
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4: /cgn2_6/prodata/1/iaa/6B_COMB_pep: *

5: /cgn2_6/prodata/1/iaa/PCMS_COMB_pep: *

6: /cgn2_6/prodata/1/iaa/bactfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	129	2	US-08-785-065-3
2	514	75.8	129	2	US-08-785-065-10
3	69.5	10.3	294	2	US-08-874-347-26
4	69.5	10.3	294	3	US-09-932-522-26
5	69	10.2	656	3	US-08-738-000-4
6	69	10.2	660	3	US-08-738-000-2
7	64	9.4	152	1	US-07-644-372-2
8	64	9.4	305	2	US-08-646-520-1
9	63	9.3	3898	4	US-08-750-717-2
10	62.5	9.2	656	2	US-08-605-106-11
11	62	9.1	214	4	US-09-587-060-6
12	61.5	9.1	60	1	US-08-370-225-32
13	61.5	9.1	60	1	US-08-611-859-32
14	61.5	9.1	60	5	PC-US91-10069-32
15	61.5	9.1	353	1	US-08-176-620A-14
16	61.5	9.1	619	2	US-08-611-938-14
17	61.5	9.1	484	2	US-08-836-620A-13
18	61.5	9.1	485	2	US-08-836-620A-2
19	61	9.0	619	2	US-08-846-767-73
20	61	9.0	619	1	US-08-472-934-4
21	61	9.0	619	1	US-08-472-934-12
22	61	9.0	619	2	US-08-472-934-12
23	61	9.0	619	2	US-08-461-145C-4
24	61	9.0	619	2	US-08-461-145C-12
25	61	9.0	619	3	US-08-461-145C-4
26	61	9.0	619	3	US-08-461-145G-12
27	9.0	915	2	US-08-480-917-2	

ALIGNMENTS

RESULT	1
US-08-785-065-3	Sequence 3, Appli
	Patent No. 5814431
	GENERAL INFORMATION:
	APPLICANT: Bandman, Olga
	APPLICANT: Hilleman, Jennifer L.
	TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
	NUMBER OF SEQUENCES: 12
	CORRESPONDENCE ADDRESS:
	ADDRESSEE: Incyte Pharmaceuticals, Inc.
	STREET: 3174 Porter Drive
	CITY: Palo Alto
	STATE: CA
	COUNTRY: USA
	ZIP: 94304
	COMPUTER READABLE FORM:
	COMPUTER: IBM Compatible
	OPERATING SYSTEM: DOS
	SOFTWARE: FastSEQ for Windows Version 2.0
	CURRENT APPLICATION DATA:
	APPLICATION NUMBER: US/08/785,065
	FILING DATE: Herewith
	CLASSIFICATION: 424
	PRIOR APPLICATION DATA:
	APPLICATION NUMBER:
	FILING DATE:
	ATTORNEY/AGENT INFORMATION:
	NAME: Billings, Lucy J.
	REGISTRATION NUMBER: 36,749
	REFERENCE/DOCKET NUMBER: PP-0187 US
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: 415-855-0555
	TELEFAX: 415-845-4166
	TELEX:
	INFORMATION FOR SEQ ID NO: 3:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 129 amino acids
	TYPE: amino acid
	STRANDEDNESS: single
	TOPOLOGY: linear
	IMMEDIATE SOURCE:
	LIBRARY: Consensus
	CLONE: Consensus
	US-08-785-065-3
	Sequence 2, Appli
	Sequence 3, Appli
	Sequence 4, Appli
	Sequence 5, Appli
	Sequence 6, Appli
	Sequence 7, Appli
	Sequence 8, Appli
	Sequence 9, Appli
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	Sequence 97, Appli
	Sequence 98, Appli
	Sequence 99, Appli
	Sequence 100, Appli

Query Match 100.0%; Score 678; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. No. 8; 7e-75; Mismatches 0; Indels 0; Gaps 0; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFPKVKPSSLRLPTELDPAEYNISPERRQAERLAIRAKLREQLLQYDNPNRGLI 60
Db 1 MSFPKVKPSSLRLPTELDPAEYNISPERRQAERLAIRAKLREQLLQYDNPNRGLI 60

QY 61 ENPALRWAYARTINVNPFRPTPKNSLMGALCGFGPLIFIVVKKTERDRKEKLQEGK 120
Db 61 ENPALRWAYARTINVNPFRPTPKNSLMGALCGFGPLIFIVVKKTERDRKEKLQEGK 120

QY 121 LDRTFHLSY 129
Db 121 LDRTFHLSY 129

RESULT 2
US-08-785-065-10
Sequence 10, Application US/08785065
FILING DATE: 08/08/2001
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
ZIP: 94304
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785, 065
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: PF-0187 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEX: 415-845-4166
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 114
US-08-785-065-10

Query Match Score 514; DB 2; Length 129;
Best Local Similarity 73.6%; Pred. No. 6; 5e-55; Indels 0; Gaps 0; Matches 95; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 1 MSFPKVKPSSLRLPTELDPAEYNISPERRQAERLAIRAKLREQLLQYDNPNRGLI 60
Db 1 MSFPKVKPSSLRLPTELDPAEYNISPERRQAERLAIRAKLREQLLQYDNPNRGLI 60

RESULT 3
US-08-874-347-26
Sequence 26, Application US/08874347
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874, 347
FILING DATE: 13 JUN 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-874-347-26

Query Match Score 69.5; DB 2; Length 294;
Best Local Similarity 36.2%; Pred. No. 1.4; Indels 1; Gaps 1; Matches 17; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 2 SFPKVKPSSLRLPTELDPAEYNISPERRQAERLAIRAKLREY 47
Db 240 AFPKWQAQDLATIVPTLDPAGLDLKMLRYEPNKRITARQALEHEY 286

RESULT 4
US-09-093-522-26
Sequence 26, Application US/09093522
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.

Db 462 EPLAETSLKEELLR--NRQGIL-----TINSOPNINGKPSSD---PIVG 503
 Qy 95 FGP--LIF--IYIYIKTERDRKEKIQ--EGKLDRFHL 127
 Db 504 WGPSSGYVFQOKAYLEFRSRETAELLQVKKVILRVNHYL 544

RESULT 7
 US-07-644-372-2
 ; Sequence 2, Application US/07644372
 ; Patent No. 541609
 ; GENERAL INFORMATION:
 ; APPLICANT: Lazzati, Mario E.
 ; APPLICANT: Nutman, Thomas B.
 ; TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 ; STREET: 1615 L Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICATION NUMBER: US/07/644,372
 FILING DATE: 1991/01/23
 CLASSIFICATION: 435
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)861-3000
 TELEFAX: (202)822-0344
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 152 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-07-644-372-2

Query Match Local Similarity 9.4%; Score 64; DB 1; Length 152; hes 26; Conservative 16; Mismatches 53; Indels 22; Gaps 3;

Qy 8 PSSLRLTPETLDPAVN----ISPETRRAQAERLAIRQLKREYLLQYNDPNRRG 58
 Db 44 PDVYSTAPTKLVNVSYNNLNTVNLNGNETPTQVKNQPTKVSWDAEPGALYTLWMTDPDAPAS 103

Qy 59 LIENPALRMRAYARITINVPNFRPTPKNSLMGALCGFPLIYIYIKTERKEK, 115
 Db 104 R-KNPVFWREHHWLINI-----SGONVSSGTVLSDYWIRKSTKRHTSSL 147

RESULT 8
 US-08-946-528-1
 ; Sequence 1, Application US/08946528
 ; Patent No. 595846
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: ELECTRON TRANSPORT PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.

RESULT 9
 US-08-750-17-2
 ; Sequence 2, Application US/08750717
 ; Patent No. 6180109
 ; GENERAL INFORMATION:
 ; APPLICANT: MOORMANN, Robertus J. M.
 ; APPLICANT: VAN RIJM, Petrus A.
 ; TITLE OF INVENTION: Nucleotide Sequences of Pestivirus Strains, Polypeptides Encoded by These Sequences and Use Thereof for Diagnosis and Prevention of Pestivirus Infections
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: YOUNG & THOMPSON
 ; STREET: 745 South 23rd Street
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,717
 FILING DATE: 24-DEC-1996
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP 94 201743.5
 FILING DATE: 17-JUN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/NL95/00214
 FILING DATE: 16-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 REFERENCE/DOCKET NUMBER: BO 39123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-521-2297
 TELEFAX: 248425 EMBON
 ; INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3898 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-750-717-2

RESULT 10
 -605-106-11
 ; Sequence 11, Application US/08605106
 ; Patent No. 5910631
 ; GENERAL INFORMATION:
 ; APPLICANT: Topfer, R.
 ; APPLICANT: Martini, N.
 ; APPLICANT: Scheil, J.
 ; TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
 ; STREET: P.O. Box 2938
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/605,106
 FILING DATE: 23-SEPT-1996
 CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP94/02935
 FILING DATE: 01-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Woessner, Warren D
 REGISTRATION NUMBER: 30,440
 REFERENCE/DOCKET NUMBER: 235.001US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-373-6900
 TELEFAX: 612-339-3061
 TELEX:
 ; INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 366 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-605-106-11

Query Match 9.3%; Score 63; DB 4; Length 3898;
 Best Local Similarity 23.0%; Pred. No. 2.8e+02; Matches 32; Conservative 19; Mismatches 44; Indels 44; Gaps 6;

Qy 2 SFPKYKPSSLRILPTEIDPAEVNISPETRRAQERLAIRQLKREYL-LOYNDPNRGLI 60
 Db 2214 SYDNYTFLNARRKLGDPPVY-----ATEDEDLAV-----ELUGLDWPUPGQNQTV 2260
 Qy 61 ENPALRWAYARTINVYPNFRPMPKNSLMGALCGFG-----PLIFIVYTIKTERD 110
 Db 2261 ETGRALKQVVGSL-----TAENALVALVALFGYVGQALSKRHHIPVVTDIYEDHR- 2310
 Qy 111 RKEKLQEGKALDRTFHLSY 129
 Db 2311 -----LEDTTHLQY 2319

RESULT 11
 US-09-587-066-6
 ; Sequence 6, Application US/09587066
 ; Patent No. 6210945
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNNEN, KEITH D.
 ; APPLICANT: MORGAN, RICHARD D.
 ; APPLICANT: MEIXSELL, TIMOTHY G.
 ; APPLICANT: WILSON, GROFFREY G.
 ; TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE RsaI RESTRICTION ENDONUCLEASE IN E. COLI AND PURIFICATION OF THE TITLE OF INVENTION: RECOMBINANT RsaI RESTRICTION ENDONUCLEASE
 FILE REFERENCE: NEB-179
 CURRENT APPLICATION NUMBER: US/09/587,066
 CURRENT FILING DATE: 2000-06-02
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Patentin Ver. 2.0
 SEO ID NO 6
 LENGTH: 214
 TYPE: RTT
 ORGANISM: rhodopseudomonas sphaeroides
 ; US-09-587-066-6

Query Match 9.1%; Score 62; DB 4; Length 214;
 Best Local Similarity 29.1%; Pred. No. 7.5; Matches 23; Conservative 10; Mismatches 38; Indels 8; Gaps 3;

Qy 11 DRTLPEIDPAEVNISPETRRAQERLAIRQLKREYLQNDPNRGLIENPA 64
 Db 83 IATIPPHL-PANNNSVAARGAGYGPDRLFVSGATRCOMEFKATSNWQDGDPNRRLVTSAPT 141
 Qy 65 -LLRWAYARTINVYPNFRP 82
 Db 142 KMIRLVNSRQGVAPNHPV 160

RESULT 12
 US-08-370-225-32
 ; Sequence 32, Application US/08370225
 ; Patent No. 580736
 ; GENERAL INFORMATION:
 ; APPLICANT: Brent, Roger

APPLICANT: Gyuris, Jeno
 APPLICANT: Golemis, Erica
 TITLE OF INVENTION: Interaction Trap System for Isolating Novel Proteins
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Wordperfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/370,225
 FILING DATE: 10/30/92
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/969,038
 FILING DATE: 10/30/92
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00786/143001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-8906
 TELEFAX: (617) 542-5070
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 60
 TYPE: amino acid
 STRANDEDNESS: linear
 TOPOLOGY: linear
 US-08-370-225-32

Query Match 9.1%; Score 61.5; DB 1; Length 60;
 Best Local Similarity 29.1%; Pred. No. 1.6; Matches 16; Conservat. 7; Mismatches 17; Indels 15; Gaps 2;
 QY 3 FPKVKPSSRLTPETL-DPAEYNISPETRRAQERLAIRQLKREYLQNDPN 55
 Dr 13 FPRVNPKGIDLQLRMLVDP-----AKRITAKEALERHPYQLYHDPN 54

RESULT 13
 US-08-461-859-32
 ; Sequence 32, Application US/08461859
 ; Patent No. 5786169
 GENERAL INFORMATION:
 APPLICANT: Brent, Roger
 APPLICANT: Gyuris, Jeno
 APPLICANT: Golemis, Erica
 TITLE OF INVENTION: Interaction Trap System for Isolating Novel Proteins
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Wordperfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US93/10069
 FILING DATE: 20-OCT-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/969,038
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 60
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

PCT-US93-10069-32

Search completed: April 29, 2001, 06:46:00
 Job time: 311 sec

Query Match 9.1%; Score 61.5; DB 5; Length 60;
 Best Local Similarity 29.1%; Pred. No. 16; Mismatches 17; Indels 15; Gaps 2;
 Matches 16; Conservative 7; Mismatches 17; Indels 15; Gaps 2;
 QY 3 FPKYKSSLRTPETL-DPAEYNISPETRRAQELAIRAQQLKREYLQYNDPN 55
 ||| : | : | | : | | : | | : | | : | | : | | : | | : | | : | |
 Db 13 FPRVNPKGIDLIQRMVFDP-----AKRITAKEALEHPYLQTYHDPN 54

RESULT 15
 US-08-176-620A-14
 Sequence 14, Application US/08176620A
 Patent No. 5595904
 GENERAL INFORMATION:
 APPLICANT: Boultton, Teri G.
 APPLICANT: Cobb, Melanie H.
 APPLICANT: Yancopoulos, George D.
 APPLICANT: Nye, Steen
 APPLICANT: Panayotatos, Nikos
 TITLE OF INVENTION: A Family of Map2 Protein Kinases
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/176,620A
 FILING DATE: 03-JAN-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9050
 TELEX: (212) 863-8864/9741
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 ; US-08-176-620A-14

Query Match 9.1%; Score 61.5; DB 1; Length 353;
 Best Local Similarity 29.1%; Pred. No. 17; Mismatches 16; Conservative 7; Mismatches 17; Indels 15; Gaps 2;
 Matches 16; Conservative 7; Mismatches 17; Indels 15; Gaps 2;
 QY 3 FPKYKSSLRTPETL-DPAEYNISPETRRAQELAIRAQQLKREYLQYNDPN 55
 ||| : | : | | : | | : | | : | | : | | : | | : | | : | |
 Db 275 FPRVNPKGIDLIQRMVFDP-----AKRITAKEALEHPYLQTYHDPN 316

Mon Apr 30 06:24:23 2001

us-09-726-899-3.rai